AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application and is presented here for convenience of the Examiner:

Listing of Claims:

1-31. (Cancelled).

32. (Currently Amended) A method, implemented by a server, for determining and presenting the likelihood a person has a mutated form of a gene, the method comprising:

receiving an electronic order from a clinician for at least one clinical agent for a person~~, wherein the electronic order does not indicate a request to use genetic techniques to characterize the person's response to the at least one clinical agent for the person~~;

in response to receiving the electronic order for the at least one clinical agent, searching a table to determine whether the at least one clinical agent is associated with a gene, the table listing a plurality of ~~genetic findings~~ genes associated with a plurality of clinical agents and clinical events;

~~in response to the electronic order~~ upon searching the table, querying a first database to determine ~~if~~ whether the person has one or more genetic test results for the gene determined to be associated with the at least one clinical agent;

~~in response to the electronic order~~ when the first database indicates that the person does not have the one or more genetic test results for the gene, ~~obtaining the mode of inheritance for the gene if the person does not have one or more genetic test results for the gene, wherein the mode of inheritance is selected~~

~~based upon the gene associated with the at least one clinical agent~~ identifying an appropriate traversal pattern of the gene within a family of the person identified, wherein the traversal pattern of the gene is identified by a process comprising:

(a) accessing an inference table that associates genes with a plurality of modes of inheritance;

(b) querying the inference table with the gene to select a mode of inheritance that corresponds with the gene; and

(c) using the selected mode of inheritance to determine the traversal pattern of the gene within the person's family;

~~utilizing the server to~~ identifying at least one family member ~~related to the person~~ within ~~a~~ the identified traversal pattern of the person's family for inspection ~~ancestors, wherein the traversal pattern is specified by the selected mode of inheritance of the gene~~;

~~without solicitation from a clinician,~~ querying a second database to determine whether at least one identified family member of the person within the traversal pattern has one or more genetic test results ~~for~~ related to the gene;

when the at least one identified family member has the one or more genetic test results for the gene, utilizing the one or more genetic test results ~~of the at least one identified family member~~ to automatically calculate a likelihood the person ~~has~~ exhibits a mutated form of the gene ~~if at least one of the family members has genetic test results for the gene~~; and

presenting the calculated likelihood the person has a mutated form of the gene to the clinician.

33. (Previously Presented) The method of claim 32, wherein the second database comprises an electronic medical record for each family member stored within a comprehensive healthcare system.

34. (Currently Amended) The method of claim 32, further comprising:

when no family member within the identified traversal pattern has the one or more genetic test results for the gene, inquiring whether the at least one identified family member of the person within the traversal pattern has one or more genetic markers related to the gene; and

when the at least one identified family member of the person within the traversal pattern has one or more genetic markers related to the gene, performing a haplotype analysis utilizing the one or more genetic markers to predict a likelihood that the person expresses a mutated form of the gene.

35. (Currently Amended) The method of claim [[34]]32, further comprising:

when no family member within the identified traversal pattern has the one or more genetic test results for the gene, determining that the person has one or more genetic findings for one or more linked genes associated with the gene; and

utilizing the one or more linked genes ~~genetic markers of at least one family member~~ of the person to calculate the likelihood the person has a mutated form of the gene.

36. (Currently Amended) The method of claim 32, further comprising providing ~~wherein the instructions for the method are embodied on~~ one or more non-transitory computer storage media configured to carry out at least one step of the method.

37. (Previously Presented) The method of claim 32, further comprising:

determining whether the mutated form of the gene is a gene variant indicative of an atypical event.

38. (Previously Presented) The method of claim 37, wherein if the mutated form of the gene is a gene variant indicative of an atypical event, presenting an alert to a user.

39. (Currently Amended) The method of claim 32, wherein the mode of inheritance is selected from one of a mitochondrial DNA mode of inheritance, an X-linked mode of inheritance, a Mendelian mode of inheritance, and a Y-linked mode of inheritance.

40. (Previously Presented) The method of claim 32 wherein said first and second databases are the same database.

41. (Currently Amended) A computer system for determining and presenting the likelihood a person has a mutated form of a gene, the computer system comprising:

a server configured to execute:

(1) a receiving module for receiving an electronic order for at least one clinical agent for a person from a clinician, wherein the electronic order does not indicate a request to use genetic techniques to characterize the person's response to the at least one clinical agent for the person;

(2) a determining module for:

(a) determining, in response to receiving the electronic order, whether the at least one clinical agent is associated with a gene, and

(b) searching an inference table to determine a maximum distance away from the gene to search for genetic findings of linked genes for the person;

(3) a first querying module for querying, in response to the electronic order, a first database to determine if the person has one or more genetic test results for the gene if the at least one clinical agent is associated with one or more genetic test results;

(4) an obtaining module for[[:]]~~(a) obtaining, in response to the electronic order, the mode of inheritance for the gene if~~ , when the person does not have the one or more genetic test results for the gene,~~ wherein the mode of inheritance is selected based upon the gene associated with the at least one clinical agent, and~~ identifying an appropriate traversal pattern of the gene within a family of the person, wherein the traversal pattern of the gene is identified by a process comprising:

(a) accessing an inference table that associates genes with a plurality of modes of inheritance;

(b) querying the inference table with the gene to select a mode of inheritance that corresponds with the gene;

(c) using the selected mode of inheritance to determine the traversal pattern of the gene within the person's family; and

(d) identifying at least one family member related to the person within ~~a~~ the identified traversal pattern of the person's family for inspection~~, wherein the traversal pattern is specified by the selected mode of inheritance of the gene~~;

(5) a second querying module for querying a second database to determine whether at least one identified family member of the person within the traversal pattern has one or more genetic test results for the gene;

(6) a utilizing module for utilizing the one or more genetic test results of the at least one family member to automatically calculate a likelihood the person has a mutated form of the gene if at least one of the family members has genetic test results for the gene; and

(7) a presenting module for presenting the calculated likelihood the person has a mutated form of the gene to the clinician without solicitation from the clinician for the calculated likelihood.

42. (Previously Presented) The system of claim 41, wherein the second database comprises an electronic medical record for each family member stored within a comprehensive healthcare system.

43. (Previously Presented) The system of claim 41, wherein the second querying module determines the mode of inheritance has one or more genetic markers related to the gene.

44. (Previously Presented) The system of claim 43, wherein the utilizing module utilizing the one or more genetic markers of at least one family member of the person to calculate the likelihood the person has a mutated form of the gene.

45. (Previously Presented) The system of claim 41, wherein the first database comprises an electronic medical record for the person.

46. (Previously Presented) The system of claim 41, further comprising:

a determining module for determining whether the mutated form of the gene is a gene variant indicative of an atypical event.

47. (Previously Presented) The system of claim 46, wherein if the mutated form of the gene is a gene variant indicative of an atypical event, the presenting module presents an alert to a user.

48. (Currently Amended) The system of claim 41, wherein the mode of inheritance is selected from one of a mitochondria1 DNA mode of inheritance, an X-linked mode of inheritance, a Mendelian mode of inheritance, and a Y-linked mode of inheritance.

49. (Currently Amended) A method, implemented by a server, for determining and presenting the likelihood a person has a mutated form of a gene, the method comprising:

receiving from a clinician an order for a medication for a person, wherein the order does not indicate a request to use genetic techniques to characterize the person's response to the medication;

in response to receiving the clinician order for medication, determining whether the order for medication is associated with a gene ~~genetic finding~~;

~~in response to the clinician order,~~ querying a first database to determine if the person has one or more genetic test results for ~~a~~ the gene ~~in response to the order for medication for a person~~;

~~in response to the electronic order~~ when the first database indicates that the person does not have the one or more genetic test results for the gene, ~~obtaining the mode of inheritance for the gene if the person does not have one or~~

~~more genetic test results for the gene, wherein the mode of inheritance is selected based upon the gene associated with the at least one clinical agent~~ identifying an appropriate traversal pattern of the gene within a family of the person identified, wherein the traversal pattern of the gene is identified by a process comprising:

(a) accessing an inference table that associates genes with a plurality of modes of inheritance;

(b) querying the inference table with the gene to select a mode of inheritance that corresponds with the gene; and

(c) using the selected mode of inheritance to determine the traversal pattern of the gene within the person's family;

~~utilizing the server to~~ identifying at least one family member ~~related to the person~~ within ~~a~~ the identified traversal pattern of the person's family for inspection ~~ancestors, wherein the traversal pattern is specified by the selected mode of inheritance of the gene~~;

~~without solicitation from a clinician,~~ querying a second database to determine whether at least one identified family member of the person within the traversal pattern has one or more genetic test results ~~for~~ related to the gene;

when the at least one identified family member has the one or more genetic test results for the gene, utilizing the one or more genetic test results to automatically calculate a likelihood the person exhibits a mutated form of the; and

~~if the patient~~ when the at least one identified family member does not have the one or more genetic test results for the gene, automatically determining whether inferred results are allowed for the gene[[,]]; ~~and if~~

when inferred results are allowed, automatically calculating an inferred finding that the ~~patient~~ person has a mutated form of the gene based, in part, on one or more genetic findings ~~associated with one or more family members of~~ expressed by the person ~~patient and also based on a Quantitative Trait Loci (QTL) analysis of the one or more genetic findings associated with the one or more family members~~, wherein the one or more genetic findings include markers linked to the gene; and

outputting the inferred finding to a display for presentation in a user-readable format within a graphical user interface (GUI).

50. (Currently Amended) The method of claim 49, further comprising ~~wherein the instructions for the method are embodied on~~ one or more non-transitory computer storage media configured to carry out at least one step of the method.

51. (Previously Presented) The method of claim 49, further comprising:

determining whether the mutated form of the gene is a gene variant indicative of an atypical event.

52. (Previously Presented) The method of claim 51, wherein if the mutated form of the gene is a gene variant indicative of an atypical event, presenting an alert to a user.